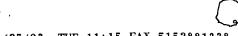


In the Claims

Please amend claims 11-14 as follows:

- (original) A method of modeling a directed evolution protocol comprising:
 applying equilibrium thermodynamics to a plurality of sequences to determine statistics of hybridization; and
 parameterizing an assembly algorithm using the statistics of hybridization.
- 2. (original) The method of claim 1 further comprising applying the assembly algorithm to reassemble a plurality of sequences.
- 3. (original) The method of claim 2 further comprising determining crossover allocation in the plurality of reassembled sequences.
- 4. (original) The method of claim 3 wherein the step of determining crossover allocation includes estimating a fraction of the plurality of reassembled sequences containing a number of crossovers.
- 5. (original) The method of claim 3 wherein the step of determining crossover allocation includes estimating a probability that a given nucleotide position in one of the plurality of reassembled sequences is a site of a crossover event.
- 6. (original) The method of claim 1 wherein the directed evolution protocol is DNA shuffling.



- The method of claim 1 wherein the directed evolution protocol is SCRATCHY. 7. (original)
- 8. (original) The method of claim 1 further comprising identifying a minimum number of required silent mutations to meet a DNA recombination objective.
- 9. (original) The method of claim 1 wherein the step of applying equilibrium thermodynamics to determine statistics of hybridization includes: modeling annealing events during reassembly as a network of reactions; determining a predicted fraction of fragments that will anneal at a given temperature; determining a predicted distribution of annealing for overlap lengths; and determining a portion of annealing events predicted to involve mismatches.
- 10. (original) The method of claim 1 wherein the assembly algorithm excludes silent crossovers.
- 11. (currently amended) An A method of providing an isolated nucleic acid molecule comprising:

providing a nucleotide sequence having an amino acid sequence; the nucleotide sequence isolated at least in part through a directed evolution experiment; and the directed evolution experiment selected at least in part by applying equilibrium thermodynamics to a plurality of sequences to determine statistics of hybridization and

parameterizing an assembly algorithm using the statistics of hybridization.

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A The method of claim 11 wherein a vector comprising comprises 12. (currently amended) the nucleic acid molecule of claim 11.

13. (currently amended)

A The method of claim 12 wherein a host cell containing contains

the vector of claim 12.

14. (currently amended)

A The method of claim 11 wherein the nucleotide sequence

encodes a protein, encoded by the nucleic acid sequence of claim 11.

15. (original)

A system for modeling a directed evolution protocol comprising:

a plurality of sequences; and

an article of software for determining statistics of hybridization of the plurality of sequences to parameterize an assembly algorithm by applying equilibrium thermodynamics to the plurality of sequences.